Figure 1

Aligned_sequences:

1: Pcan057

2: Pcan057v1 # Matrix: EDNAFULL .# Gap_penalty: 100.0 # Extend_penalty: 0.05 50 1 aaacttcatcaaggtacntaaggttgtaaggttctcggggggtagcggct Pcan057 Pcan057v1 . 51 tgcacacctcttgaagggcttcarccgggcccctggctccttcaggctgg 100 Pcan057 Pcan057v1 150 101 ctgccttnatccgcttatccaatgattggataacggatgaggggagtctg Pcan057 0 1 Pcan057v1 200 151 ggtgccaggtgctttgcccgcatggcccatttcagtcacgctgcagtcct Pcan057 Pcan057v1 250 201 gtcaggaaaaaatcagtgttattctcattctacatatgagaaaactgagg Pcan057 0. Pcan057vl 1 300 Pcan057 ٥ 1 Pcan057v1 350 301 agtttcagactccacagtctcttaaccaccaagcagcatgcccagagtag Pcan057 1 Pcan057v1 351 aggtgagaaggaaggagagctgcggtccacatgagcatctggacctag 400 Pcan057 ٥ Pcan057v1 1 450 401 catggacaactcactcctcctggctctcgctttgttcttgttgcgggtg Pcan057 0 1 Pcan057v1 451 tggtggtggtgggactcaaagacggtaaagatagctttctctcccctg 500 Pcan057 1 Pcan057v1 501 gggaatctgggggttgtttaaaaggcctgctcctcttttagaaggcagga 550 Pcan057 0 Pcan057v1

		, - 5
Pcan057	551 gggccccaagggaagcagaaggtgacagaaggggaaagggtcctctgatc	600
Pcan057v1		0
Pcan057	601 attgctc	607
Pcan057v1	1 aattetegagetegtegaeeggtegaegagetegagggtegaegageteg	·50
Pcan057	608	607
Pcan057v1	51 agggcgcgcgccccgcccccccccccccccccgcgcccc	100
Pcan057	608	607
Pcan057v1	101 tcccagccgggtccagccggagccatggggccggagccgcagtgagcacc	150
Pcan057	608	607
Pcan057v1	151 atggagetggeggeettgtgeegetgggggeteeteetegeeetettgee	200
Pcan057	608	607
Pcan057v1	201 ccccggagccgcgagcacccaagtgtgcaccggcacagacatgaagctgc	250
Pcan057	608	607
Pcan057v1	251 ggctccctgccagtcccgagacccacctggacatgctccgccacctctac	300
Pcan057	608	607
Pcan057v1	301 cagggctgccaggtggtgcagggaaacctggaactcacctacct	350
Pcan057	608	607
Pcan057v1	351 caatgccagcctgtccttcctgcaggatatccaggaggtgcagggctacg	400
Pcan057	608	607
Pcan057v1	401 tgctcatcgctcacaaccaagtgaggcaggtcccactgcagaggctgcgg	450
Pcan057	608	607
Pcan057vl	451 attgtgcgaggcacccagctctttgaggacaactatgccctggccgtgct	500
Pcan057	608	607
Pcan057v1	501 agacaatggagacccgctgaacaataccacccctgtcacaggggcctccc	550

Pcan057	608accccacagagatcttgaaa 6	27
Pcan057v1		0∙0 `
Pcan057		77
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Pcan057v1		00
Pcan057	828 cactgtctgtgccggtggctgtgcccgctgcaaggggccactgcccactg 8	77
Pcan057v1		50
Pcan057	878 actgctgccatgagcagtgtgctgccggctgcacgggccccaagcactct 9	27
Pcan057v1		00
Pcan057	928 gactgcctgcctccacttcaaccacagtggcatctgtgagctgca 9	77
Pcan057v1		50
Pcan057	978 ctgccagcctggtcacctacaacacagacacgtttgagtccatgccca 10	27
Pcan057v1	• • • • • • • • • • • • • • • • • • • •	00
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Pcan057v1		.050
Pcan057	1078 tacaactacctttctacggacgtgggatcctgcaccctcgtctgccccct 1	127
Pcan057v1		100
Pcan057	1128 gcacaaccaagaggtgacagcagaggatggaacacagcggtgtgagaagt	L 1 77
Pcan057v1		150
Pcan057	1178 gcagcaagccctgtgcccgagtgtgctatggtctgggcatggagcacttg	1227
Pcan057v1		200

•			. 0,
Pcan057		caccagtgccaatatccaggagttigctggcts	1277
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Pcan057vl		gcccgctccagccagagcagctccaagtgtt	
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Pcan057		gcgtcttccagaacctgcaagtaatccggggad	
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Pcan057		ctcactgaggaactgggcagtggactggccc	
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Pcan057	578 catccaccataacaccc	acctctgcttcgtgcacacggtgccctgggac	c 1627
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Pcan057	.678 gaggacgagtgt		- 1689
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Pcan057	.690	·	- 1689
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Pcan057	.690		- 1689

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Pcan057			1689
Pcan057v1	1851	gratecttecetececetetgtttetgaaateteagaactetteetete	1900
Pcan057	1690		1689
Pcan057v1	1901	ctacateggccccacctgtccccaccctccagcccacagccatgcccac	1950
Pcan057	1690		1689
Pcan057v1		agccagttccctggttcacttggacctggggcctcccctaaaagtcccct	2000
Pcan057	1690	gtgggcgagggcctggcctgccaccag	1716
Pcan057v1	2001	geggteeetteeteeteactgeagtgggegagggeetggeet	2050
Pcan057	1717	ctgtgcgcccgagggcactgctggggtccagggcccaccca	1766
Pcan057v1	2051	ctgtgcgcccgagggcactgctggggtccagggcccaccca	2100
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Pcan057v1	2101	ctgcagccagttccttcggggccaggagtgcgtggaggaatgccgagtac	2150
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Pcan057	2067	cacccactcctgtgtggacctggatgacaagggctgccccgccgagcaga	2116
Pcan057v1	2401	cacccactcctgtgtggacctggatgacaagggctgccccgccgagcaga	2450

••			
Pcan057	•	gagccagccctctgacgtccatcatctctgcggtggttggcattctgctg	216 6
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Pcan057 g	2167	gtcgtggtcttgggggtggtctttgggatcctcatcaagcgacggcagca	2216
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Pcan057v1	2751	aaattccagtggccatcaaagtgttgagggaaaacacatccccaaagcc	2800
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Pcan057vl	3451	cagggaccccagcgctttgtggtcatccagaatgaggacttgggcccag	3500
Pcan057	3167	ccagtcccttggacagcaccttctaccgctcactgctggaggacgatgac	3216
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Pcan057	3217	atgggggacctggtggatgctgaggagtatctggtaccccagcagggctt	3266
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Pcan057v1	3601	cttctgtccagaccctgccccgggcgctgggggcatggtccaccacaggc	3650
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Pcan057v1	3651	accgcagctcatctaccaggagtqqcqgtqgggacctgacactagggctg	3700

	•	A Company of the Comp	
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Pcan057v1	3801	ggctgcaaagcctcccacacatgaccccagccctctacagcggtacagt	3850
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Pcan057vl	3851	gaggacccacagtacccctgccctctgagactgatggctacgttgcccc	3900
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Pcan057v1	3951	cccagccccttcgcccgagagggccctctgcctgctgccgacctgct	4000
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Pcan057v1	4001		4050
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Pcan057	3917	agtacctgggtctggacgtgccagtgtgaaccagaaggccaagtccgcag	3966
Pcan057v1	4251	agtacctgggtctggacgtgccagtgtgaaccagaaggccaagtccgcag	4300
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Pcan057v1	4301	aagccctgatgtgtcctcagggagcagggaaggcctgacttctgctggca	4350

Pcan057	4017	tcaagaggtgggaġggccctccgaccacttccaggggaacctgccatgcc	4066
Pcan057v1	4351	tcaagaggtgggagggcctccgaccacttccaggggaacctgccatgcc	4400
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Pcan057v1	4751	gtttagtttttactttttttgttttgtttttttaaagatgaaataaagac	4800
Pcan057	4467		4516
Pcan057v1	4801	ccagggggagaatgggtgttgtatggggaggcaagtgtggggggtccttc	4850
Pcan057	4517	tccacacccactttgtccatttgcaaatatattttggaaaaca 4559	
Pcan057v1	4851	tccacacccactttgtccatttgcaaatatattttggaaaaca 4893	

Figure 2

# Aligned_seq	uenc	es: 2	•
# 1:° Pcan057.	aa		
# 2: Pcan057v	1.aa		
# Matrix: EBL	OSUM	162	
# Gap_penalty	: 10	0.0	
# Extend_pena	lty:	0.01	
#========	====	=======================================	
,			_
Pcan057.aa	1		0
Pcan057v1.aa	. 1	MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLY	50
Pcan057.aa	1		0
Pcan057v1.aa	51	QGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLR	100
Pcan057.aa	1	MGLSFRLHSLLTTKQ: .	15
Pcan057v1.aa	101	IVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSL	145
Pcan057.aa	16	HAQSRGEKEGESCGPHEHLDLAWTTHSSLALALFLLRVWWWWDSKTVKIA	65
Pcan057v1.aa	146		14,5
Pcan057.aa		FSPPWGIWGLFKRPAPLLEGRRAPREAEGDRRGKGPLIIAHPTEILKGGV	115
Pcan057v1.aa	146		153
Pcan057.aa	116	LIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSR	165
Pcan057vl.aa	154	LIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSR	203
Pcan057.aa	166	CWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCL	215
Pcan057v1.aa	204	CWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCL	253
Pcan057.aa	216	ACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY	26
Pcan057v1.aa	254	ACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY	30:
Pcan057.aa	266	LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREV	31
Pcan057vl.aa	304	LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREV	35
Pcan057.aa	316	RAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETL	36
Pcan057v1.aa	354	RAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETL	40

Pcan057.aa	 366	EEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWL	415
• •		EEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWL	453
Pcan057.aa	416	GERSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDE	465
Pcan057v1.aa	454	GLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDE	503
Pcan057.aa	466	CVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPRE	515
Pcan057v1.aa	504	CGKTGSPVCALPICQHTAVPRGPWQQRSWTCADCPSLCTLLDSAQLWLAW	553
Pcan057.aa	516	YVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSG	565
Pcan057v1.aa	554	PLGMASLAGSYLPWHPSLPLCF	575
Pcan057.aa	566	VKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS	615
Pcan057v1.aa	576		575
Pcan057.aa	616	IISAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPS	665
Pcan057v1.aa	576		575
Pcan057.aa	666	GAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIK	715
Pcan057v1.aa	576		575
Pcan057.aa	716	VLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPY	765
Pcan057v1.aa	576	•	575
Pcan057.aa	766	GCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLV	815
Pcan057v1.aa	576		575
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Pcan057v1.aa	576		575
Pcan057.aa	866	DVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYM	915
Pcan057v1.aa	576		575
Pcan057.aa	916	IMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDST	965
Pcan057v1.aa	576		575
Pcan057.aa	966	FYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTR	1015

Pcan057v1.aa	a 576		57.5
Pcan057.aa	1016	SGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPT	1065
Pcan057v1.a	a 576		575
Pcan057.aa	1066	HDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPR	1115
Pcan057v1.aa	a 576		575
Pcan057.aa	1116	egplpaarpagatleraktlspgkngvvkdvfafggavenpeyltpggga	1165
Pcan057v1.a	a 576		575
Pcan057.aa	1166	APQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDV	1215
Pcan057v1.a	a 576		575
Pcan057.aa	1216	PV 1217	
Pcan057v1.a	a 576	575	

Figure 3.

		,	
Pro108	1		6
Pro177	1	gggagggataggacggggagacaaagaaaggggtgcggcagcactgccag	50
Pro108	7	gggaagagggtgatccgacccggggaaggtcgctgggcagggcgagttgg	56
Pro177	51	gggaagagggtgatccgacccggggaaggtcgctgggcagggcgagttgg	100
Pro108	57	gaaageggcageeeeggeeeeggcageeeetteteeteet	106
Pro177	101	gaaageggeageceegeegeeeegeageceetteteeteet	150
Pro108	107	acgtectatetgeetetegetggaggeeaggeegtgeageategaagaea	156
Pro177	151	acgtcctatctgcctctcgctggaggccaggccgtgcagcatcgaagaca	200
Pro108	. 157	ggaggaactggagcctcattggccggcccggggcgccggcctcgggctta	206
Pro177	201	ggaggaactggagcctcattggccggcccgggcgccggcctcgggctta	250
Pro108	207	aataggageteegggetetggetgggaceegacegetgeeggeegegete	256
Pro177	251	aataggageteegggetetggetgggaceegacegetgeeggeegete	300
Pro108	257	ccgctgctcctgccgggtgatggaaaaccccagcccggccgccctgg	306
Pro177	301	. ccgctgctcctgccgggtgatggaaaaccccagcccggccgccctgg	350
Pro108	307	gcaaggccctctgcgctctcctcctggccactctcggcgccgccggccag	356
Pro177	351	. gcaaggccctctgcgctctcctcctggccactctcggcgccgccggccag	400
Pro108	357	cctcttgggggagagtccatctgttccgccagagccccggccaaatacag	406
Pro177	401	cctcttgggggagagtccatctgttccgccagagccccggccaaatacag	450
Pro108	407	catcaccttcacgggcaagtggagccagacggccttccccaagcagtacc	456
Pro177	451	catcaccttcacgggcaagtggagccagacggccttccccaagcagtacc	500
Prol08	457	ccctgttccgccccctgcgcagtggtcttcgctgctgggggccgcgcat	506
•		441111111111111111111111111111111111111	

Pro177	501	ccctgttccgccccctgcgcagtggtcttcgctgctgggggccgcgcat	550
Pro108	507	agctccgactacagcatgtggaggaagaaccagtacgtcagtaacgggct	556
Pro177	551	agetecgaetacageatgtggaggaagaaccagtacgtcagtaacggget	600
`Pro108	557	gcgcgactttgcggagcgcggcgaggcctgggcgctgatgaaggagatcg	606
Pro177	601	gcgcgactttgcggagcgcggcgaggcctgggcgctgatgaaggagatcg	650
Pro108	607	aggcggcgggggaggcgctgcagagcgtgcacgcggtgttttcggcgccc	656
Pro177	651	aggeggegggggggegetgeagagegtgcaegaggtgtttteggegeee	700
Pro108		gccgtccccagcggcaccgggcagacgtcggcggagctggaggtgcagcg	706
Pro177	701	gccgtccccagcggcaccgggcagacgtcggcggagctggaggtgcagcg	750
Pro108	707	caggcactcgctggtctcgtttgtggtgcgcatcgtgcccagccccgact	756
Pro177	751	caggcactegetggtetegtttgtggtgcgcatcgtgcccagcccgact	800
Pro108	757	ggttcgtgggcgtggacagcctggacctgtgcgacggggaccgttggcgg	806
Pro177	801	ggttcgtgggcgtggacagcctggacctgtgcgacggggaccgttggcgg	850
Pro108	807	gaacaggcggcgctggacctgtacccctacgacgccgggacggac	856
Pro177	851	gaacaggcggctggacctgtacccctacgacgccgggacggac	900
Prol08	857	cttcaccttctcctccccaacttcgccaccatcccgcaggacacggtga	906
Pro177	901	cttcaccttctcctccccaacttcgccaccatcccgcaggacacggtga	950
Pro108	907	ccgagataacgtcctctctcccagccacccggccaactccttctactac	956
Prol77	951	ccgagataacgtcctcctctcccagccacccggccaactccttctactac	1000
Prol08	957	ccgcggctgaaggccctgcctcccatcgccagggtgacactggtgcggct	1006
Pro177	1001	ccgcggctgaaggccctgcctcccatcgccagggtgacactgctgcggct	1050
Pro108	1007	gcgacagagccccagggccttcatccctcccgccccagtcctgcccagca	1056
Pro177	1051	gcgacagagccccagggccttcatccctcccgcccagtcctgcccagca	1100
Pro108	1057	gggacaatgagattgtagacagcgcct	1083
Pro177	1101	gggacaatgagattgtagacagcgcctcaggtaacggacatacaggtcac	1150

Pro108	1084		1083
Pro177		atgggacacacagcagcccgaaccctgccacagggcgaccaccaaaccc	1200
Pro108	1084		1083
Pro177		gaacctaaggctctgagaaattccaagtagggattcgtagtgcgtactgc	1250
Pro108	1084		1083
Pro177	1251	aagatggtgcctagaagatttaggattctgttgattcacacactgaagat	1300
Pro108	1084		1083
Pro177	1301	gtgactcttgcacattatttgcagttgaaagcatcttacagggccacagc	1350
Pro108	1084		1083
Pro177	1351	ccagaggaaagaatgaaaggaggctccagacagtacctgagagactctgt	1400
Pro108	1084		1083
Pro177	1401	cctgtcagacacgcacccacaggtgacctgtgtgtcacagctgacaagga	1450
Pro108	1084		1083
Pro177	1451	agettgetaggatggecetgtgtggccacegggtgacagetatgetgeag	15,00
Pro108	1084		1083
Pro177	1501	ggcacctgtgggggtctcgggacccagccaccacacagctcggggctctg	1550
Pro108	1084		1083
Pro177	1551	ctcacaggcgccttggcctggggcggggcaggtgctgatgagcattctcc	1600
Pro108	1084		1083
Pro177	1601	tagctcttccaggcacctgctggacagggcaggctgggaacgctggggcc	1650
Pro108	1084		1083
Pro177	1651	gagtggcagttccctccctactcagctgggtggcagccactggcctcacg	1700
Pro108	1084		1083
Pro177	1701	gagcgcctgtggtctggagcgcattgctgggtcgtgggtcagggcctgtt	1750
Pro108	1084		1083

Pro177	1751	ggetetgggtetetgggteteacetgatatgggtgtgggacagteagtgt	1800
Pro108	1084		1083
Pro177	1801	aggccccagacaacagcggacttcagactttcccgaggaggaactggagc	1850
Pro108	1084		1083
Pro177	1851	ccaccaacctggccatgggccccgtcgtcctccaccttccatgttgctgg	1900
Pro108	1084		1083
Pro177	1901	ctggagttgaggcaggtacggggccgcccacacctgcccccaagccat	1950
Pro108	1084		1083
Pro177	1951	gtggtagggacagatgtcgtcttgaggagcagcagtaattacaagcttac	2000
Pro108	1084		1083
Pro177	2001	tgtcagccgtccctggaagcaaggccaggtcaggtcagacaggaggccg	2050
Pro108	1084		1083
Pro177	2051	cctggctggcgggaaccactccccagacagagactgtgcccagtcctggg	2100
Pro108	1084		1083
Pro177	2101	tccctcctcatttgggatgaactgggcctccctgtgccagcctcggtgct	2150
Pro108	1084		1083
Pro177	2151	gcccctgcccagtgcaggcttgggctcctcactcatttgtccacgcggat	2200
Pro108	1084		1083
Pro177		gccccattccaagcagatgtccccgagccacttacccaacaggcagacgt	2250
Pro108	1084		1083
Pro177	2251	gccagcactgttcgtggtgtgcaactggtctggcgggaagagcccctcgt	2300
Pro108	1084		1083
Pro177	2301	gggcagagggtccagaggtgcggtttgccccacatttgggggcactgg	2350
Pro108	1084		1083
Pro177	2351	gccacagtgggcaggggagcacgtggccagtgccctgggtctgccacgat	2400

Pro108	1084		1083
Pro177	2401	gtgggagttccaccaccagggacttgagcggcagctccggctcttacg	2450
Pro108	1084		1083
Pro177	2451	tagaaacgcgcaactccagtccctaggttgtgtccgaggttgctatggtg	2500
Pro108	1084		1083
Pro177	2501	ccatcccatcttgccgctcactctgcgactgtgcggagaaacgcaagtgc	2550
Pro108	1084		1083
Pro177	2551	ccccgaagggtgggcgtggcctctgatgaatgcacacgttggtgggaggt	2600
Pro108	1084		1083
Pro177	2601	ggcttccgtttgtacgaagcgcctcttcacgcgagcgttcacctcggtct	2650
Pro108	1084	cagttccagaaacgccgctggactgcgaggtctcc	1118
Pro177	2651	ccctttgcttggtccagttccagaaacgccgctggactgcgaggtctcc	2700
Pro108	1119	ctgtggtcgtcctggggactgtgcggaggccactgtgggaggctcgggac	1168
Pro177	2701	ctgtggtcgtcctggggactgtgcggaggccactgtgggaggctcgggac	2750
Pro108	1169	caagagcaggactcgctacgtccgggtccagcccgccaacaacgggagcc	1218
Pro177	2751	caagagcaggactcgctacgtccgggtccagcccgccaacaacgggagcc	2800
Pro108	1219	cctgccccgagctcgaagaagaggctgagtgcgtccctgataactgcgtc	1268
Pro177	2801	cctgccccgagctcgaagaagaggctgagtgcgtccctgataactgcgtc	2850
Pro108	1269	taagaccagagccccgcagcccctgggg-cccccggagccatggggtgtc	1317
Pro177	2851	taagaccagagccccgcagcccctggggccccccggagccatggggtgtc	2900
Pro108	1318	gggggctcctgtgcaggctcatgctgcaggcggccga-ggcacagggggt	1366
Pro177	2901	gggggctcctgtgcaggctcatgctgcaggcgggccgagggcacagggggt	2950
Pro108	1367	ttcgcgctgctcctgaccgcggtgaggccgcgccgaccatctctgcactg	1416
Pro177	2951	ttcgcgctgctcctgaccgcggtgaggccgcgccgaccatctctgcactg	3000

Pro108	1417	aagggccctctggtggccggcacgggcattgggaaacagcctccttt	2466
Pro177	3001	aagggccctctggtggccggcacgggcattgggaaacagcctcctctt	3050
Pro108	1467	cccaaccttgcttcttaggggccccgtgtcccgtctgctctcagcctcc	1516
Pro177	3051	cccaaccttgcttcttaggggcccccgtgtcccgtctgctctcagcctcc	3100
Pro108	1517	tcctcctgcaggataaagtcatccccaaggctccagctactctaaattat	1566
Pro177	3101	tectectgeaggataaagteateceeaaggeteeagetactetaaattat	3150
Pro108	1567	ggtctccttataagttattgctgctccaggagattgtccttcatcgtcca	1616
Pro177	3151	-gtctccttataagttattgctgctccaggagattgtccttcatcgtcca	3199
Pro108	1617	ggggcetggetcceacgtggttgcagatacctcagacctggtgctctagg	1666
Pro177	3200	ggggcctggctcccacgtggttgcagatacctcagacctggtgctctagg	3249
Pro108	1667	ctgtgctgagcccactctcccgagggcgcatccaagcgggggccacttga	1716
Pro177	3250	ctgtgctgagcccactctcccgagggcgcatccaagcgggggccacttga	3299
Pro108	1717	gaagtgaataaatggggcggtttcggaagcgtcagtgtttccatgttatg	1766
Pro177	3300	gaagtgaataaatggggcggtttcggaagcgtcagtgtttccatgttatg	3349
Pro108	1767	gatctctctgcgtttgaataaagactatctctgttgctcac 1807	
Pro177	3350	 gatctctctgcgtttgaataaagactatctctgttgctcaaaaa 3393	

Figure 4

Aligned_seq # 1: PRO108 # 2: PRO177 # Matrix: E # Gap_penal # Extend_pe	.aa .aa BLOS ty: nalt	SUM62 100.0 :y: 0.01					·		•	
PRO108.aa	1	MENPSPAAALO	KALC	ALLLA:	rlgaago	PLGGE	SICSAI	RAPAK'	YSITFTG	sk 50
PRO177.aa	1	MENPSPAAAL	KALC	ALLLA'	rlgaago	PLGGE	SICSA	RAPAK	YSITFTO	5K 50
PRO108.aa	· 51	WSQTAFPKQY	PLFRP:	PAQWS:	SLLGAAH	SSDYS	MWRKN	QYVSN	GLRDFAE	R 100
PRO177.aa	51	WSQTAPPKQY	PLFRP	PAQWS	SLLGAAE	ISSDYS	MWRKN	OYVSN	GLRDFA	100
PRO108.aa	101	GEAWALMKEI:	EAAGE.	ALQSV	HAVFSAI	AVPSG	TGQTS	AELEV	QRRHSL\	7S 150
PRO177.aa	101	GEAWALMKEI:	EAAGE.	ALQSV.	HEVFSA	AVPSG	TGQTS.	AELEV	QRRHSL	7S 150
PRO108.aa	151	FVVRIVPSPD	WFVGV	DSLDL	CDGDRWE	REQAAL	DLYPY	DAGTD	SGFTFS:	SP 200
PRO177.aa	151	FVVRIVPSPD	WFVGV	DSLDL	CDGDRWI	REQAAL	DLYPY	DAGTD	SGFTFS	SP 200
PRO108.aa	201	NFATIPQDTV	TEITS	SSPSH	PANSFY	PRLKA	LPPIA	RVTLV	RLRQSPI	RA 250
PRO177.aa	201	NFATIPQDTV	TEITS	SSPSH	PANSFY	ZPRLKA	LPPIA	RVTLL	RLRQSPI	RA 250
PRO108.aa	251	FIPPAPVLPS	RDNEI	VDSAS	VPETPLI	CEVSI	WSSWG	LCGGH	CGRLGT	KS 300
PRO177.aa	251	FIPPAPVLPS	RDNEI	VDSAS	GNGHTGI	IMGHTA	APNPA	TGRPP	NPNLRL	298
PRO108.aa	301	RTRYVRVQPA	nngsp	CPELE	EEAECV	PDNCV	33	1		
PRO177.aa	299						29	8		٠

Figure 5

# Aligned_sequences: 2 # 1: PRO108.aa # 2: PRO177.orf # Matrix: EBLOSUM62 # Gap_penalty: 100.0 # Extend_penalty: 0.01	
#======================================	
PRO108.aa 1	0
PRO177.orf 1 RCDSCTLFAVESILQGHSPEERMKGGSRQYLRDSVLSDTHPQVTCVSQLT	50
PRO108.aa 1	0
PRO177.orf 51 RKLARMALCGHRVTAMLQGTCGGLGTQPPHSSGLCSQAPWPGAGQVLMSI	100
PRO108.aa 1	0
PRO177.orf 101 LLALPGTCWTGQAGNAGAEWQFPPYSAGWQPLASRSACGLERIAGSWVRA	150
PRO108.aa 1	0
PRO177.orf 151 CWLWVSGSHLIWVWDSQCRPQTTADFRLSRGGTGAHQPGHGPRRPPPSML	200
PRO108.aa 1	0
PRO177.orf 201 LAGVEAGTGPPHTCPPSHVVGTDVVLRSSSNYKLTVSRPWKQGPGQVRQE	250
PRO108.aa 1	(
PRO177.orf 251 AAWLAGTTPQTETVPSPGSLLIWDELGLPVPASVLPLPSAGLGSSLICPR	300
PRO108.aa 1	(
PRO177.orf 301 GCPIPSRCPRATYPTGRRASTVRGVQLVWREEPLVGRGSREVRFAPHLGA	350
PRO108.aa 1	(
PRO177.orf 351 LGHSGQGSTWPVPWVCHDVGVPPPQGLERQLRLLRRNAQLQSLGCVRGCY	400
PRO108.aa 1	:
PRO177.orf 401 GAIPSCRSLCDCAEKRKCPRRVGVASDECTRWWEVASVCTKRLFTRAFTS	45
PRO108.aa 4 PSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQ .	5
PRO177.orf 451 VSPLL	45
PRO108.aa 54 TAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEA	103

PRO108.aa	 54	TAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEA	103
			455
PRO108.aa	104	WALMKEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVSFVV	153
PRO177.orf	456		455
PRO108.aa	154	RIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGFTFSSPNFA	203
PRO177.orf	456		455
PRO108.aa	204	TIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLVRLRQSPRAFIP	253
PRO177.orf	456		455
PRO108.aa	254	PAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTR	303
PRO177.orf	456		490
PRO108.aa	304	YVRVQPANNGSPCPELEEEAECVPDNCV 331	
PRO177.orf	491		